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OIIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,830

DATE: 01/08/2002

TIME: 14:41:35

Input Set : N:\Crf3\RULE60\09965830.raw

Output Set: N:\CRF3\01082002\I965830.raw

1 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
 2 <120> TITLE OF INVENTION: A novel potassium channel protein
 3 <130> FILE REFERENCE: Y9903-PCT
 4 <140> CURRENT APPLICATION NUMBER: 09/965,830
 5 <141> CURRENT FILING DATE: 2001-10-01
 6 <150> PRIOR APPLICATION NUMBER: 09/600,776
 7 <151> PRIOR FILING DATE: 2000-07-21
 8 <150> PRIOR APPLICATION NUMBER: JP P1998-346198
 9 <151> PRIOR FILING DATE: 1998-12-04

ENTERED

10 <160> NUMBER OF SEQ ID NOS: 12
 11 <170> SOFTWARE: PatentIn Ver. 2.0

13 <210> SEQ ID NO: 1

14 <211> LENGTH: 3323

15 <212> TYPE: DNA

16 <213> ORGANISM: Homo sapiens

17 <220> FEATURE:

18 <221> NAME/KEY: CDS

19 <222> LOCATION: (6)..(3257)

20 <400> SEQUENCE: 1

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24   gac acc atc gct acg cgc ttc gac ggc acg cac agt aac ttc gtg ctg   98
25   Asp Thr Ile Ala Thr Arg Phe Asp Gly Thr His Ser Asn Phe Val Leu
26           20             25             30
27   ggc aac gcc cag gtg gcg ggg ctc ttc ccc gtg gtc tac tgc tct gat   146
28   Gly Asn Ala Gln Val Ala Gly Leu Phe Pro Val Val Tyr Cys Ser Asp
29           35             40             45
30   ggc ttc tgt gac ctc acg ggc ttc tcc cgg gct gag gtc atg cag cgg   194
31   Gly Phe Cys Asp Leu Thr Gly Phe Ser Arg Ala Glu Val Met Gln Arg
32           50             55             60
33   ggc tgt gcc tgc tcc ttc ctt tat ggg cca gac acc agt gag ctc gtc   242
34   Gly Cys Ala Cys Ser Phe Leu Tyr Gly Pro Asp Thr Ser Glu Leu Val
35           65             70             75
36   cgc caa cag atc cgc aag gcc ctg gac gag cac aag gag ttc aag gct   290
37   Arg Gln Gln Ile Arg Lys Ala Leu Asp Glu His Lys Glu Phe Lys Ala
38           80             85             90             95
39   gag ctg atc ctg tac cgg aag agc ggg ctc ccg ttc tgg tgt ctc ctg   338
40   Glu Leu Ile Leu Tyr Arg Lys Ser Gly Leu Pro Phe Trp Cys Leu Leu
41           100            105            110
42   gat gtg ata ccc ata aag aat gag aaa ggg gag gtg gct ctc ttc cta   386
43   Asp Val Ile Pro Ile Lys Asn Glu Lys Gly Glu Val Ala Leu Phe Leu
44           115            120            125
45   gtc tct cac aag gac atc agc gaa acc aag aac cga ggg ggc ccc gac   434
46   Val Ser His Lys Asp Ile Ser Glu Thr Lys Asn Arg Gly Gly Pro Asp
47           130            135            140
48   aga tgg aag gag aca ggt ggt ggc cgg cgc cga tat ggc cgg gca cga   482

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49	Arg	Trp	Lys	Glu	Thr	Gly	Gly	Gly	Arg	Arg	Arg	Tyr	Gly	Arg	Ala	Arg	
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51	tcc	aaa	ggc	ttc	aat	gcc	aac	cgg	cgg	cgg	agc	cgg	gcc	gtg	ctc	tac	530
52	Ser	Lys	Gly	Phe	Asn	Ala	Asn	Arg	Arg	Arg	Ser	Arg	Ala	Val	Leu	Tyr	
53		160					165				170					175	
54	cac	ctg	tcc	ggg	cac	ctg	cag	aag	cag	ccc	aag	ggc	aag	cac	aag	ctc	578
55	His	Leu	Ser	Gly	His	Leu	Gln	Lys	Gln	Pro	Lys	Gly	Lys	His	Lys	Leu	
56					180					185					190		
57	aat	aag	ggg	gtg	ttt	ggg	gag	aaa	cca	aac	ttg	cct	gag	tac	aaa	gta	626
58	Asn	Lys	Gly	Val	Phe	Gly	Glu	Lys	Pro	Asn	Leu	Pro	Glu	Tyr	Lys	Val	
59				195					200					205			
60	gcc	gcc	atc	cgg	aag	tcg	ccc	ttc	atc	ctg	ttg	cac	tgt	ggg	gca	ctg	674
61	Ala	Ala	Ile	Arg	Lys	Ser	Pro	Phe	Ile	Leu	Leu	His	Cys	Gly	Ala	Leu	
62			210					215					220				
63	aga	gcc	acc	tgg	gat	ggc	ttc	atc	ctg	ctc	gcc	aca	ctc	tat	gtg	gct	722
64	Arg	Ala	Thr	Trp	Asp	Gly	Phe	Ile	Leu	Leu	Ala	Thr	Leu	Tyr	Val	Ala	
65		225					230				235						
66	gtc	act	gtg	ccc	tac	agc	gtg	tgt	gtg	agc	aca	gca	cgg	gag	ccc	agt	770
67	Val	Thr	Val	Pro	Tyr	Ser	Val	Cys	Val	Ser	Thr	Ala	Arg	Glu	Pro	Ser	
68		240				245				250					255		
69	gcc	gcc	cgc	ggc	ccg	ccc	agc	gtc	tgt	gac	ctg	gcc	gtg	gag	gtc	ctc	818
70	Ala	Ala	Arg	Gly	Pro	Pro	Ser	Val	Cys	Asp	Leu	Ala	Val	Glu	Val	Leu	
71				260					265					270			
72	ttc	atc	ctt	gac	att	gtg	ctg	aat	ttc	cgt	acc	aca	ttc	gtg	tcc	aag	866
73	Phe	Ile	Leu	Asp	Ile	Val	Leu	Asn	Phe	Arg	Thr	Thr	Phe	Val	Ser	Lys	
74		275						280					285				
75	tcg	ggc	cag	gtg	gtg	ttt	gcc	cca	aag	tcc	att	tgc	ctc	cac	tac	gtc	914
76	Ser	Gly	Gln	Val	Val	Phe	Ala	Pro	Lys	Ser	Ile	Cys	Leu	His	Tyr	Val	
77		290						295				300					
78	acc	acc	tgg	ttc	ctg	ctg	gat	gtc	atc	gca	gcg	ctg	ccc	ttt	gac	ctg	962
79	Thr	Thr	Trp	Phe	Leu	Leu	Asp	Val	Ile	Ala	Ala	Leu	Pro	Phe	Asp	Leu	
80		305				310					315						
81	cta	cat	gcc	ttc	aag	gtc	aac	gtg	tac	ttc	ggg	gcc	cat	ctg	ctg	aag	1010
82	Leu	His	Ala	Phe	Lys	Val	Asn	Val	Tyr	Phe	Gly	Ala	His	Leu	Leu	Lys	
83		320			325					330					335		
84	acg	gtg	cgc	ctg	ctg	cgc	ctg	ctg	cgc	ctg	ctt	ccg	cgg	ctg	gac	cgg	1058
85	Thr	Val	Arg	Leu	Leu	Arg	Leu	Leu	Arg	Leu	Leu	Pro	Arg	Leu	Asp	Arg	
86			340					345					350				
87	tac	tcg	cag	tac	agc	gcc	gtg	gtg	ctg	aca	ctg	ctc	atg	gcc	gtg	ttc	1106
88	Tyr	Ser	Gln	Tyr	Ser	Ala	Val	Val	Leu	Thr	Leu	Leu	Met	Ala	Val	Phe	
89			355					360				365					
90	gcc	ctg	ctc	gcg	cac	tgg	gtc	gcc	tgc	gtc	tgg	ttt	tac	att	ggc	cag	1154
91	Ala	Leu	Leu	Ala	His	Trp	Val	Ala	Cys	Val	Trp	Phe	Tyr	Ile	Gly	Gln	
92		370					375					380					
93	cgg	gag	atc	gag	agc	agc	gaa	tcc	gag	ctg	cct	gag	att	ggc	tgg	ctg	1202
94	Arg	Glu	Ile	Glu	Ser	Ser	Glu	Ser	Glu	Leu	Pro	Glu	Ile	Gly	Trp	Leu	
95		385				390					395						
96	cag	gag	ctg	gcc	cgc	cga	ctg	gag	act	ccc	tac	tac	ctg	gtg	ggc	cgg	1250
97	Gln	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Thr	Pro	Tyr	Tyr	Leu	Val	Gly	Arg	

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98	400	405	410	415	
99	agg cca gct gga ggg aac agc tcc ggc cag agt gac aac tgc agc agc				1298
100	Arg Pro Ala Gly Gly Asn Ser Ser Gly Gln Ser Asp Asn Cys Ser Ser				
101		420	425	430	
102	agc agc gag gcc aac ggg acg ggg ctg gag ctg ctg ggc ggc ccg tcg				1346
103	Ser Ser Glu Ala Asn Gly Thr Gly Leu Glu Leu Leu Gly Gly Pro Ser				
104		435	440	445	
105	ctg cgc agc gcc tac atc acc tcc ctc tac ttc gca ctc agc agc ctc				1394
106	Leu Arg Ser Ala Tyr Ile Thr Ser Leu Tyr Phe Ala Leu Ser Ser Leu				
107		450	455	460	
108	acc agc gtg ggc ttc ggc aac gtg tcc gcc aac acg gac acc gag aag				1442
109	Thr Ser Val Gly Phe Gly Asn Val Ser Ala Asn Thr Asp Thr Glu Lys				
110		465	470	475	
111	atc ttc tcc atc tgc acc atg ctc atc ggc gcc ctg atg cac gcg gtg				1490
112	Ile Phe Ser Ile Cys Thr Met Leu Ile Gly Ala Leu Met His Ala Val				
113		480	485	490	495
114	gtg ttt ggg aac gtg acg gcc atc atc cag cgc atg tac gcc cgc cgc				1538
115	Val Phe Gly Asn Val Thr Ala Ile Ile Gln Arg Met Tyr Ala Arg Arg				
116		500	505	510	
117	ttt ctg tac cac agc cgc acg cgc gac ctg cgc gac tac atc cgc atc				1586
118	Phe Leu Tyr His Ser Arg Thr Arg Asp Leu Arg Asp Tyr Ile Arg Ile				
119		515	520	525	
120	cac cgt atc ccc aag ccc ctc aag cag cgc atg ctg gag tac ttc cag				1634
121	His Arg Ile Pro Lys Pro Leu Lys Gln Arg Met Leu Glu Tyr Phe Gln				
122		530	535	540	
123	gcc acc tgg gcg gtg aac aat ggc atc gac acc acc gag ctg ctg cag				1682
124	Ala Thr Trp Ala Val Asn Asn Gly Ile Asp Thr Thr Glu Leu Leu Gln				
125		545	550	555	
126	agc ctc cct gac gag ctg cgc gca gac atc gcc atg cac ctg cac aag				1730
127	Ser Leu Pro Asp Glu Leu Arg Ala Asp Ile Ala Met His Leu His Lys				
128		560	565	570	575
129	gag gtc ctg cag ctg cca ctg ttt gag gcg gcc agc cgc ggc tgc ctg				1778
130	Glu Val Leu Gln Leu Pro Leu Phe Glu Ala Ala Ser Arg Gly Cys Leu				
131		580	585	590	
132	cgg gca ctg tct ctg gcc ctg cgg ccc gcc ttc tgc acg ccg ggc gag				1826
133	Arg Ala Leu Ser Leu Ala Leu Arg Pro Ala Phe Cys Thr Pro Gly Glu				
134		595	600	605	
135	tac ctc atc cac caa ggc gat gcc ctg cag gcc ctc tac ttt gtc tgc				1874
136	Tyr Leu Ile His Gln Gly Asp Ala Leu Gln Ala Leu Tyr Phe Val Cys				
137		610	615	620	
138	tct ggc tcc atg gag gtg ctc aag ggt ggc acc gtg ctc gcc atc cta				1922
139	Ser Gly Ser Met Glu Val Leu Lys Gly Gly Thr Val Leu Ala Ile Leu				
140		625	630	635	
141	ggg aag ggc gac ctg atc ggc tgt gag ctg ccc cgg cgg gag cag gtg				1970
142	Gly Lys Gly Asp Leu Ile Gly Cys Glu Leu Pro Arg Arg Glu Gln Val				
143		640	645	650	655
144	gta aag gcc aat gcc gac gtg aag ggg ctg acg tac tgc gtc ctg cag				2018
145	Val Lys Ala Asn Ala Asp Val Lys Gly Leu Thr Tyr Cys Val Leu Gln				
146		660	665	670	

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147	tgt ctg cag ctg gct ggc ctg cac gac agc ctt gcg ctg tac ccc gag	2066
148	Cys Leu Gln Leu Ala Gly Leu His Asp Ser Leu Ala Leu Tyr Pro Glu	
149	675 680 685	
150	ttt gcc ccg cgc ttc agt cgt ggc ctc cga ggg gag ctc agc tac aac	2114
151	Phe Ala Pro Arg Phe Ser Arg Gly Leu Arg Gly Glu Leu Ser Tyr Asn	
152	690 695 700	
153	ctg ggt gct ggg gga ggc tct gca gag gtg gac acc agc tcc ctg agc	2162
154	Leu Gly Ala Gly Gly Gly Ser Ala Glu Val Asp Thr Ser Ser Leu Ser	
155	705 710 715	
156	ggc gac aat acc ctt atg tcc acg ctg gag gag aag gag aca gat ggg	2210
157	Gly Asp Asn Thr Leu Met Ser Thr Leu Glu Glu Lys Glu Thr Asp Gly	
158	720 725 730 735	
159	gag cag ggc ccc acg gtc tcc cca gcc cca gct gat gag ccc tcc agc	2258
160	Glu Gln Gly Pro Thr Val Ser Pro Ala Pro Ala Asp Glu Pro Ser Ser	
161	740 745 750	
162	ccc ctg ctg tcc cct ggc tgc acc tcc tca tcc tca gct gcc aag ctg	2306
163	Pro Leu Leu Ser Pro Gly Cys Thr Ser Ser Ser Ser Ala Ala Lys Leu	
164	755 760 765	
165	cta tcc cca cgt cga aca gca ccc cgg cct cgt cta ggt ggc aga ggg	2354
166	Leu Ser Pro Arg Arg Thr Ala Pro Arg Pro Arg Leu Gly Gly Arg Gly	
167	770 775 780	
168	agg cca ggc agg gca ggg gct ttg aag gct gag gct ggc ccc tct gct	2402
169	Arg Pro Gly Arg Ala Gly Ala Leu Lys Ala Glu Ala Gly Pro Ser Ala	
170	785 790 795	
171	ccc cca cgg gcc cta gag ggg cta cgg ctg ccc ccc atg cca tgg aat	2450
172	Pro Pro Arg Ala Leu Glu Gly Leu Arg Leu Pro Pro Met Pro Trp Asn	
173	800 805 810 815	
174	gtg ccc cca gat ctg agc ccc agg gta gta gat ggc att gaa gac ggc	2498
175	Val Pro Pro Asp Leu Ser Pro Arg Val Val Asp Gly Ile Glu Asp Gly	
176	820 825 830	
177	tgt ggc tcg gac cag ccc aag ttc tct ttc cgc gtg ggc cag tct ggc	2546
178	Cys Gly Ser Asp Gln Pro Lys Phe Ser Phe Arg Val Gly Gln Ser Gly	
179	835 840 845	
180	ccg gaa tgt agc agc agc ccc tcc cct gga cca gag agc ggc ctg ctc	2594
181	Pro Glu Cys Ser Ser Ser Pro Ser Pro Gly Pro Glu Ser Gly Leu Leu	
182	850 855 860	
183	act gtt ccc cat ggg ccc agc gag gca agg aac aca gac aca ctg gac	2642
184	Thr Val Pro His Gly Pro Ser Glu Ala Arg Asn Thr Asp Thr Leu Asp	
185	865 870 875	
186	aag ctt cgg cag gcg gtg aca gag ctg tca gag cag gtg ctg cag atg	2690
187	Lys Leu Arg Gln Ala Val Thr Glu Leu Ser Glu Gln Val Leu Gln Met	
188	880 885 890 895	
189	cgg gaa gga ctg cag tca ctt cgc cag gct gtg cag ctt gtc ctg gcg	2738
190	Arg Glu Gly Leu Gln Ser Leu Arg Gln Ala Val Gln Leu Val Leu Ala	
191	900 905 910	
192	ccc cac agg gag ggt ccg tgc cct cgg gca tcg gga gag ggg ccg tgc	2786
193	Pro His Arg Glu Gly Pro Cys Pro Arg Ala Ser Gly Glu Gly Pro Cys	
194	915 920 925	
195	cca gcc agc acc tcc ggg ctt ctg cag cct ctg tgt gtg gac act ggg	2834

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199   Ala Ser Ser Tyr Cys Leu Gln Pro Pro Ala Gly Ser Val Leu Ser Gly
200           945           950           955
201   act tgg ccc cac cct cgt ccg ggg cct cct ccc ctc atg gca ccc tgg   2930
202   Thr Trp Pro His Pro Arg Pro Gly Pro Pro Pro Leu Met Ala Pro Trp
203   960           965           970           975
204   ccc tgg ggt ccc cca gcg tct cag agc tcc ccc tgg cct cga gcc aca   2978
205   Pro Trp Gly Pro Pro Ala Ser Gln Ser Ser Pro Trp Pro Arg Ala Thr
206           980           985           990
207   gct ttc tgg acc tcc acc tca gac tca gag ccc cct gcc tca gga gac   3026
208   Ala Phe Trp Thr Ser Thr Ser Asp Ser Glu Pro Pro Ala Ser Gly Asp
209           995           1000           1005
210   ctc tgc tct gag ccc agc acc cct gcc tcc cct cct cct tct gag gaa   3074
211   Leu Cys Ser Glu Pro Ser Thr Pro Ala Ser Pro Pro Pro Ser Glu Glu
212           1010           1015           1020
213   ggg gct agg act ggg ccc gca gag cct gtg agc cag gct gag gct acc   3122
214   Gly Ala Arg Thr Gly Pro Ala Glu Pro Val Ser Gln Ala Glu Ala Thr
215           1025           1030           1035
216   agc act gga gag ccc cca cca ggg tca ggg ggc ctg gcc ttg ccc tgg   3170
217   Ser Thr Gly Glu Pro Pro Pro Gly Ser Gly Gly Leu Ala Leu Pro Trp
218   1040           1045           1050           1055
219   gac ccc cac agc ctg gag atg gtg ctt att ggc tgc cat ggc tct ggc   3218
220   Asp Pro His Ser Leu Glu Met Val Leu Ile Gly Cys His Gly Ser Gly
221           1060           1065           1070
222   acà gtc cag tgg acc cag gaa gaa ggc aca ggg gtc tga gtaccagccc   3267
223   Thr Val Gln Trp Thr Gln Glu Glu Gly Thr Gly Val
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229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
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235           20           25           30
236   Asn Ala Gln Val Ala Gly Leu Phe Pro Val Val Tyr Cys Ser Asp Gly
237           35           40           45
238   Phe Cys Asp Leu Thr Gly Phe Ser Arg Ala Glu Val Met Gln Arg Gly
239           50           55           60
240   Cys Ala Cys Ser Phe Leu Tyr Gly Pro Asp Thr Ser Glu Leu Val Arg
241           65           70           75           80
242   Gln Gln Ile Arg Lys Ala Leu Asp Glu His Lys Glu Phe Lys Ala Glu
243           85           90           95
244   Leu Ile Leu Tyr Arg Lys Ser Gly Leu Pro Phe Trp Cys Leu Leu Asp
245           100           105           110

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VERIFICATION SUMMARY

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